

## Identification of New Genes in Wheat and Barley for Stripe Rust Resistance

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Stripe rust of wheat, caused by *Puccinia striiformis* f. sp. *tritici*, is historically most destructive in the western United States and has become increasingly important in the Great Plains and southeastern states. Barley stripe rust, caused by *P. striiformis* f. sp. *hordei*, has become an important disease in the western U.S. since the early 1990s. The diseases are best controlled by growing resistant cultivars. The rapid changes of new races in the rust pathogens make numerous genes for race-specific all-stage (seedling) resistance ineffective. Although high-temperature, adult-plant (HTAP) resistance is non-race-specific and therefore, durable, this type of resistance may not be adequate in some locations and years when the weather conditions are favorable to stripe rust and rust pressure is high. Therefore, the best approach is to combine genes for HTAP resistance and effective all-stage resistance to develop cultivars with durable and high-level resistance.

Resistant wheat and barley genotypes were identified through germplasm evaluation in various field locations under natural infection and in greenhouse with selected races of the pathogens covering all possible virulences. Genotypes with resistance controlled by potential new genes were crossed with susceptible barley or wheat lines to develop progeny populations for genetic analysis and molecular mapping. Mapping populations were phenotyped in the seedling stage under controlled greenhouse inoculation conditions and/or at adult-plant stages under field natural infection conditions, depending upon the type of resistance. The resistance gene analog polymorphism (RGAP) and simple sequence repeat (SSR) techniques were used to identify markers associated with resistance genes. Amplification of the Chinese Spring nulli-tetrasomic lines or the wheat and barley additional lines with suitable RGAP markers was used to identify chromosomes carrying resistance genes. Chromosome-specific SSR markers were used to confirm chromosomes and identify chromosomal regions of resistance genes. Chromosomal locations, race reactions, and types of resistance were used to identify new genes. Amplification of various wheat or barley genotypes with markers flanking resistance genes were used to validate the markers and determine the usefulness of markers in marker-assisted selection.

We have mapped a recessive gene in ‘Grannenlose Zweizeilige’ on chromosome 4HL and a recessive gene in ‘BBA 2890’ barley on chromosome 3HL for all-stage resistance. A quantitative trait locus (QTL) with a major effect for HTAP resistance in ‘Bancroft’ barley was mapped on chromosome 3HL. *Yr36* conferring HTAP resistance was identified from *Triticum turgidum* spp. *dicoccoides* and mapped on wheat chromosome 6BS. The *Yr39* HTAP resistance gene in ‘Alpowa’ spring wheat was mapped on 7BL. A QTL for HTAP resistance in ‘AVS/6\*Yr8’ wheat line was identified and mapped on 2DL. A QTL for HTAP resistance in ‘Stephen’ winter wheat was mapped on 6BS, closely linked to the *Yr36* locus. Three QTL for HTAP resistance in ‘Express’ spring wheat mapped on 6AS, 3BL, and 1BL are distinct from the previously reported genes. *YrAlp* in Alpowa and *YrExp1* and *YrExp2* in Express for race-specific all-stage resistance were mapped on 1BS, 1BL, and 5BL, respectively. *YrExp2* is different from previously reported *Yr* genes. These genes and their flanking markers should be useful in developing cultivars with durable and adequate resistance to stripe rust.